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SEQUENCE LISTING

<110> Hayward, Nicholas K.
Weber, Gunther
Grimmond, Sean
Nordenskjold, Magnus
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING SAME

<130> DAVIES

<140> 08/765,588
<141> 1996-02-22

<160> 23

<170> PatentIn Ver. 2.0

<210> 1
<211> 649
<212> DNA
<213> Nucleotide Sequence of VEGF165

<220>
<221> CDS
<222> (17)..(589)

<400> 1

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tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt 52
                  Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
                    1               5                  10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc   100
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
         15                  20                  25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg   148
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
     30                  35                  40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac   196
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 45                  50                  55                  60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc   244
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
```

```
                65                  70                  75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg   292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
            80                  85                  90

gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg   340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
        95                  100                 105

atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag   388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
    110                 115                 120

cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa   436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
125                 130                 135                 140

aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa   484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
                145                 150                 155

gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc   532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
            160                 165                 170

aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag   580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
        175                 180                 185

ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg           629
Pro Arg Arg
    190

gaaccagatc tctcaccagg                                            649


<210> 2
<211> 191
<212> PRT
<213> Nucleotide Sequence of VEGF165

<400> 2
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
  1               5                  10                  15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
            20                  25                  30
```

```
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
         35                  40                  45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
     50                  55                  60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65                  70                  75                  80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
                 85                  90                  95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
            100                 105                 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
        115                 120                 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
    130                 135                 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145                 150                 155                 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
                165                 170                 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
            180                 185                 190
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A3 cont.

<210> 3
<211> 1094
<212> DNA
<213> Nucleotide Sequence of SOM175

<220>
<221> CDS
<222> (3)..(623)

<400> 3

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cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag    47
   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
     1               5                  10                  15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
```

```
                  20                  25                  30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
             35                  40                  45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
         50                  55                  60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
     65                  70                  75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80                  85                  90                  95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg   335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
                100                 105                 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa   383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
            115                 120                 125

aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac   431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
        130                 135                 140

cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca   479
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
    145                 150                 155

ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct   527
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
160                 165                 170                 175

gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc   575
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
                180                 185                 190

gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct   623
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
            195                 200                 205

tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683
```

a3 cont.

agactcagca gggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743

tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803

ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863

agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923

tggagtactg tctcagtttc taaccactct gtgcaagtaa gcatcttaca actggctctt 983

cctcccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tggtacaaga 1043

actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4
<211> 207
<212> PRT
<213> Nucleotide Sequence of SOM175

<400> 4

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
  1               5                  10                  15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
             20                  25                  30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
         35                  40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
     50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                 85                  90                  95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
            100                 105                 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115                 120                 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
    130                 135                 140
```

a3 cont.

```
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
145                 150                 155                 160

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
                165                 170                 175

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
            180                 185                 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
        195                 200                 205
```

<210> 5
<211> 993
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exon 6

<220>
<221> CDS
<222> (3)..(566)

<400> 5

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cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag    47
   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
     1               5                  10                  15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
                20                  25                  30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
            35                  40                  45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
        50                  55                  60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
    65                  70                  75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80                  85                  90                  95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg   335
```

a3 cont.

```
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
                100                 105                 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa   383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
            115                 120                 125

aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca   431
Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
        130                 135                 140

cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc   479
Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
    145                 150                 155

cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag   527
Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
160                 165                 170                 175

ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg    576
Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
                180                 185

cttttcagac tcagcagggt gacttgcctc agaggctata tcccagtggg ggaacaaagg 636

ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag 696

gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tccctgaggc catcatcaaa 756

caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816

ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876

gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt gggctttggt 936

acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa    993


<210> 6
<211> 188
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
  1               5                  10                  15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
```

```
            20                  25                  30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
         35                  40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
     50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                 85                  90                  95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
            100                 105                 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115                 120                 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
    130                 135                 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145                 150                 155                 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
                165                 170                 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
            180                 185
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a3 cont.

<210> 7
<211> 858
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
<221> CDS
<222> (3)..(431)

<400> 7

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cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag    47
   Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
     1               5                  10                  15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95
```

```
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
                 20                  25                  30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
             35                  40                  45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
         50                  55                  60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
     65                  70                  75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80                  85                  90                  95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg   335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
                100                 105                 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa   383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
            115                 120                 125

aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg   431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
        130                 135                 140
```

a3 cont

```
tgacacatgg cttttcagac tcagcagggt gacttgcctc agaggctata tcccagtggg 491

ggaacaaagg ggagcctggt aaaaaacagc caagccccca agacctcagc ccaggcagaa 551

gctgctctag gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tccctgaggc 611

catcatcaaa caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata 671

ccagctcagg ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat 731

cttacaactg gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt 791

gggctttggt acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa 851

aaaaaaa                                                          858
```

<210> 8
<211> 143
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140

A3 Cont

<210> 9
<211> 910
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
<221> CDS
<222> (3)..(305)

<400> 9
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
1 5 10 15

```
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac   95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
                20                  25                  30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc   143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
            35                  40                  45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc   191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
        50                  55                  60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt   239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
    65                  70                  75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac   287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80                  85                  90                  95

caa gtc cgg atg cag acc taaaaaaaag gacagtgctg tgaagccaga          335
Gln Val Arg Met Gln Thr
                100

cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395

ccccggagca ccctccccag ctgacatcac ccatcccact ccagccccag gcccctctgc 455

ccacgctgca cccagcacca ccagcgccct gacccccgga cctgccgctg ccgctgccga 515

cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaacccaga cacctgcagg 575

tgccggaagc tgcgaaggtg acacatggct tttcagactc agcagggtga cttgcctcag 635

aggctatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695

cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755

ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815

gcaagagggg tcacatacca gctcagggga gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaactggct cttcc                            910
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<210> 10
<211> 101
<212> PRT

<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
  1               5                  10                  15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
             20                  25                  30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
         35                  40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
     50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                 85                  90                  95

Val Arg Met Gln Thr
            100
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<210> 11
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 11
accaccacct ccctgggctg gcatgtggca cgtgcataaa cg 42

a3 cont

<210> 12
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 12
agttgtttga ccacattgcc catgagttcc atgctcagag gc 42

<210> 13
<211> 38
<212> DNA
<213> Oligonucleotide

<400> 13
gatcctgggg ctggagtggg atggatgatg tcagctgg 38

<210> 14
<211> 40
<212> DNA
<213> Oligonucleotide

<400> 14
gcgggcagag gatcctgggg ctgtctggcc tcacagcact 40

<210> 15
<211> 236
<212> DNA
<213> Human SOM175

<400> 15
atgaggggcc aggtacgtga ggtctcccac aggcccctgg aaagaatact tacatctgct 60

cccatggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagtcttt ctcctccgta ggctgcctcc agccccaggc 180

cccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16
<211> 1242
<212> DNA
<213> mVRF

a3 cont.

<220>
<221> CDS
<222> (166)..(831)

<400> 16
gcacgagctc aggccgtcgc tgcggcgctg cgttgcgctg cctgcgccca gggctcggga 60

gggggccgcg gaggagccgc cccctgcgcc ccgccccggg tccccgggtc cgcgccatgg 120

ggcggctctg gctgaccccc ccccacaccg ccgggctagg gcccg atg agc ccc ctg 177
Met Ser Pro Leu
1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225
Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu Ala Arg Thr Gln

```
  5                  10                  15                  20

gcc cct gtg tcc cag ttt gat ggc ccc agt cac cag aag aaa gtg gtg   273
Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln Lys Lys Val Val
                25                  30                  35

cca tgg ata gac gtt tat gca cgt gcc aca tgc cag ccc agg gag gtg   321
Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln Pro Arg Glu Val
            40                  45                  50

gtg gtg cct ctg agc atg gaa ctc atg ggc aat gtg gtc aaa caa cta   369
Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val Val Lys Gln Leu
        55                  60                  65

gtg ccc agc tgt gtg act gtg cag cgc tgt ggt ggc tgc tgc cct gac   417
Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys Cys Pro Asp
    70                  75                  80

gat ggc ctg gaa tgt gtg ccc act ggg caa cac caa gtc cga atg cag   465
Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val Arg Met Gln
85                  90                  95                  100

atc ctc atg atc cag tac ccg agc agt cag ctg ggg gag atg tcc ctg   513
Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly Glu Met Ser Leu
                105                 110                 115

gga gaa cac agc caa tgt gaa tgc aga cct aaa aaa aag gag agt gct   561
Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys Glu Ser Ala
            120                 125                 130

gtg agg cca gac agg gtt gcc ata ccc cac cac cgt ccc cag ccc cgc   609
Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg
        135                 140                 145

tct gtt ccg ggc tgg gac tct acc ccg gga gca ccc tcc cca gct gac   657
Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp
    150                 155                 160

atc atc cat ccc act cca gcc cca gga tcc tct gcc cgc ctt gca ccc   705
Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro
165                 170                 175                 180

agc gcc gcc aac gcc ctg acc ccc gga cct gcc gtt gcc gct gta gac   753
Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp
                185                 190                 195

gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agc tca acc cag   801
Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala     Ser Ser Thr Gln
```

a3 cont.

200 205 210

aca cct gta ggt gcc gga agc cgc gaa agt gacaagctgc tttccagact 851
Thr Pro Val Gly Ala Gly Ser Arg Glu Ser
215 220

ccacgggccc ggctgctttt atggccctgc ttcacaggga gaagagtgga gcacaggcgt 911

aacctcctca gtctgggagg tcactgcccc aggacctgga ccttttagag agctctctcg 971

ccatctttta tctcccagag ctgccatcta acaattgtca aggaacctca tgtctcacct 1031

caggggccag ggtactctct cacttaacca ccctggtcaa gtgagcatct tctggctggc 1091

tgtctcccct cactatgaaa accccaaact tctaccaata acgggatttg ggttctgtta 1151

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1242

<210> 17
<211> 207
<212> PRT
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<400> 17
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
1 5 10 15

Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
20 25 30

Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
50 55 60

Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
100 105 110

a3 cont.

Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro
145 150 155 160

Ser Pro Ala Asp Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala
165 170 175

Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val
180 185 190

Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
195 200 205

<210> 18
<211> 14
<212> PRT
<213> mVRF

<400> 18
Ser Ser Thr Gln Thr Pro Val Gly Ala Gly Ser Arg Glu Ser
1 5 10

<210> 19
<211> 188
<212> PRT
<213> mVRF167

<400> 19
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
1 5 10 15

Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
20 25 30

Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
50 55 60

Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly

a3 cont.

```
 65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85                  90                  95

Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
            100                 105                 110

Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
        115                 120                 125

Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro
    130                 135                 140

Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145                 150                 155                 160

Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu
                165                 170                 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys
            180                 185
```

<210> 20
<211> 188
<212> PRT
<213> hVRF167

<400> 20

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
  1               5                  10                  15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
            20                  25                  30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
        35                  40                  45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
    50                  55                  60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65                  70                  75                  80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
                85                  90                  95
```

A3 cont

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 21
<211> 71
<212> PRT
<213> mVRF186

<400> 21
Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15

Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro
20 25 30

Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn
35 40 45

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser
50 55 60

Ser Ile Ala Lys Gly Gly Ala
65 70

a3 cont.

<210> 22
<211> 71
<212> PRT
<213> hVRF186

<400> 22
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly

```
  1               5                  10                  15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
             20                  25                  30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
         35                  40                  45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ala Ser
     50                  55                  60

Ser Val Ala Lys Gly Gly Ala
 65                  70
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<210> 23
<211> 214
<212> PRT
<213> mVEGF188

<400> 23

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Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
  1               5                  10                  15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
             20                  25                  30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
         35                  40                  45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
     50                  55                  60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
 65                  70                  75                  80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
                 85                  90                  95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
            100                 105                 110

Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
        115                 120                 125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg
    130                 135                 140
```

a3 cont.

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys
145 150 155 160

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu
165 170 175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp
180 185 190

A3 cont

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
195 200 205

Cys Asp Lys Pro Arg Arg
210